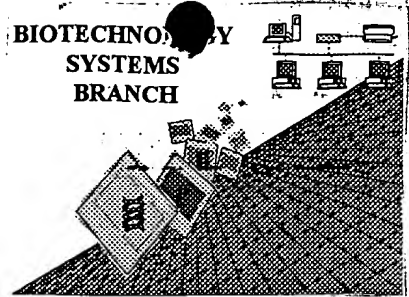


Q. Nguyen

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/578,656  
Source: 1632  
Date Processed by STIC: 11/30/2000

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Q. Nguyen

#4  
12-14-00  
1632 P. Z

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/578,656  
DATE: 11/30/2000  
TIME: 11:00:20

Input Set : A:\4910-3-SequenceListing.txt  
Output Set: N:\CRF3\11302000\I578656.raw

Does Not Comply  
Corrected Diskette Needed

4 <110> APPLICANT: Li, Hung  
5 Hsieh-Li, Hsiu-Mei  
6 Chang, Jan-Gowth  
7 Jong, Yuh-Jyh  
8 Wu, Mei-Hsiang  
9 Tsai, Chang-Hai  
11 <120> TITLE OF INVENTION: A Knockout-Transgenic Mouse Model of Spinal Muscular Atrophy  
W--> 12 <130> FILE REFERENCE: 4910-3  
W--> 13 <140> CURRENT APPLICATION NUMBER: US 09/578,656  
14 <141> CURRENT FILING DATE: 2000-05-25  
15 <150> PRIOR APPLICATION NUMBER: US 60/136,520  
16 <151> PRIOR FILING DATE: 1999-05-28  
W--> 17 <160> NUMBER OF SEQ ID: 15

ERRORED SEQUENCES

19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 21  
21 <212> TYPE: DNA  
22 <213> ORGANISM: Artificial Sequence  
W--> 23 <220> FEATURE:  
24 <223> OTHER INFORMATION: Primer for PCR  
W--> 25 <400> SEQUENCE: 1  
E--> 26 ataacaccac cactttact c  
29 <210> SEQ ID NO: 2  
30 <211> LENGTH: 21  
31 <212> TYPE: DNA  
32 <213> ORGANISM: Artificial Sequence  
W--> 33 <220> FEATURE:  
34 <223> OTHER INFORMATION: Primer for PCR  
W--> 35 <400> SEQUENCE: 2  
E--> 36 gtagecgtga tgccattgtc a  
39 <210> SEQ ID NO: 3  
40 <211> LENGTH: 21  
41 <212> TYPE: DNA  
42 <213> ORGANISM: Artificial Sequence  
W--> 43 <220> FEATURE:  
44 <223> OTHER INFORMATION: Primer for PCR  
W--> 45 <400> SEQUENCE: 3  
E--> 46 agcctgaaga acgagatcag c  
48 <210> SEQ ID NO: 4  
49 <211> LENGTH: 24  
50 <212> TYPE: DNA  
51 <213> ORGANISM: Artificial Sequence  
W--> 52 <220> FEATURE:  
53 <223> OTHER INFORMATION: Primer for PCR

Per 1.822 of Sequence Rules,  
insert cumulative base total  
at right margin of  
each line

21

21

21

global error

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/578,656

DATE: 11/30/2000  
 TIME: 11:00:20

Input Set : A:\4910-3-SequenceListing.txt  
 Output Set : N:\CRF3\11302000\1578656.raw

W--> 54 <400> SEQUENCE: 4  
 E--> 55 actgcaacct cctgggttca agtg  
 58 <210> SEQ ID NO: 5  
 59 <211> LENGTH: 24  
 60 <212> TYPE: DNA  
 61 <213> ORGANISM: Artificial Sequence  
 W--> 62 <220> FEATURE:  
 63 <223> OTHER INFORMATION: Primer for PCR  
 W--> 64 <400> SEQUENCE: 5  
 E--> 65 cagttcgaga ccagcctgac caat  
 68 <210> SEQ ID NO: 6  
 69 <211> LENGTH: 25  
 70 <212> TYPE: DNA  
 71 <213> ORGANISM: Artificial Sequence  
 W--> 72 <220> FEATURE:  
 73 <223> OTHER INFORMATION: Primer for PCR  
 W--> 74 <400> SEQUENCE: 6  
 E--> 75 cgaatcactt gagggcagga gtttg  
 78 <210> SEQ ID NO: 7  
 79 <211> LENGTH: 25  
 80 <212> TYPE: DNA  
 81 <213> ORGANISM: Artificial Sequence  
 W--> 82 <220> FEATURE:  
 83 <223> OTHER INFORMATION: Primer for PCR  
 W--> 84 <400> SEQUENCE: 7  
 E--> 85 aactggtgga catggctggt cattg  
 88 <210> SEQ ID NO: 8  
 89 <211> LENGTH: 25  
 90 <212> TYPE: DNA  
 91 <213> ORGANISM: Artificial Sequence  
 W--> 92 <220> FEATURE:  
 93 <223> OTHER INFORMATION: Primer for PCR  
 W--> 94 <400> SEQUENCE: 8  
 E--> 95 aaaccagtcg ggcacaatac ctacg  
 98 <210> SEQ ID NO: 9  
 99 <211> LENGTH: 24  
 100 <212> TYPE: DNA  
 101 <213> ORGANISM: Artificial Sequence  
 W--> 102 <220> FEATURE:  
 103 <223> OTHER INFORMATION: Primer for PCR  
 W--> 104 <400> SEQUENCE: 9  
 E--> 105 tatgctgatt gaaggagggt gtgc  
 108 <210> SEQ ID NO: 10  
 109 <211> LENGTH: 28  
 110 <212> TYPE: DNA  
 111 <213> ORGANISM: Artificial Sequence  
 W--> 112 <220> FEATURE:  
 113 <223> OTHER INFORMATION: Primer for PCR  
 W--> 114 <400> SEQUENCE: 10

24 ← insert

24

insert  
 cumulative  
 base totals  
 globally

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/578,656  
 DATE: 11/30/2000  
 TIME: 11:00:20

Input Set : A:\4910-3-SequenceListing.txt  
 Output Set : N:\CRF3\11302000\i578656.raw

```

E--> 115 cgctgcgcac ccgcgggttt gctatggc
      118 <210> SEQ ID NO: 11
      119 <211> LENGTH: 21
      120 <212> TYPE: DNA
      121 <213> ORGANISM: Artificial Sequence
W--> 122 <220> FEATURE:
      123 <223> OTHER INFORMATION: Primer for PCR
W--> 124 <400> SEQUENCE: 11
E--> 125 tcccagtcctt gccctggca t
      128 <210> SEQ ID NO: 12
      129 <211> LENGTH: 20
      130 <212> TYPE: DNA
      131 <213> ORGANISM: Artificial Sequence
W--> 132 <220> FEATURE:
      133 <223> OTHER INFORMATION: Primer for PCR
W--> 134 <400> SEQUENCE: 12
E--> 135 aacatcaagc ccaaatctgc
      138 <210> SEQ ID NO: 13
      139 <211> LENGTH: 29
      140 <212> TYPE: DNA
      141 <213> ORGANISM: Artificial Sequence
W--> 142 <220> FEATURE:
      143 <223> OTHER INFORMATION: Primer for PCR
W--> 144 <400> SEQUENCE: 13
E--> 145 gccagtatga tagccactca tgtaccatg
      148 <210> SEQ ID NO: 14
      149 <211> LENGTH: 31
      150 <212> TYPE: DNA
      151 <213> ORGANISM: Artificial Sequence
W--> 152 <220> FEATURE:
      153 <223> OTHER INFORMATION: Primer for PCR
W--> 154 <400> SEQUENCE: 14
E--> 155 ctcccatatg tccagattct cttgatgatg c
      158 <210> SEQ ID NO: 15
      159 <211> LENGTH: 21
      160 <212> TYPE: DNA
      161 <213> ORGANISM: Artificial Sequence
W--> 162 <220> FEATURE:
      163 <223> OTHER INFORMATION: Primer for PCR
W--> 164 <400> SEQUENCE: 15
E--> 165 actgcctcac caccgtgctg g

```

*insert  
base totals  
globally*

## VERIFICATION SUMMARY

DATE: 11/30/2000

PATENT APPLICATION: US/09/578,656

TIME: 11:00:21

Input Set : A:\4910-3-SequenceListing.txt

Output Set: N:\CRF3\11302000\I578656.raw

L:12 M:283 W: Missing Blank Line separator, <130> field identifier  
L:13 M:283 W: Missing Blank Line separator, <140> field identifier  
L:17 M:283 W: Missing Blank Line separator, <160> field identifier  
L:23 M:283 W: Missing Blank Line separator, <220> field identifier  
L:25 M:283 W: Missing Blank Line separator, <400> field identifier  
L:26 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:1  
L:33 M:283 W: Missing Blank Line separator, <220> field identifier  
L:35 M:283 W: Missing Blank Line separator, <400> field identifier  
L:36 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:2  
L:43 M:283 W: Missing Blank Line separator, <220> field identifier  
L:45 M:283 W: Missing Blank Line separator, <400> field identifier  
L:46 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:3  
L:52 M:283 W: Missing Blank Line separator, <220> field identifier  
L:54 M:283 W: Missing Blank Line separator, <400> field identifier  
L:55 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:4  
L:62 M:283 W: Missing Blank Line separator, <220> field identifier  
L:64 M:283 W: Missing Blank Line separator, <400> field identifier  
L:65 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:5  
L:72 M:283 W: Missing Blank Line separator, <220> field identifier  
L:74 M:283 W: Missing Blank Line separator, <400> field identifier  
L:75 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:6  
L:82 M:283 W: Missing Blank Line separator, <220> field identifier  
L:84 M:283 W: Missing Blank Line separator, <400> field identifier  
L:85 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:7  
L:92 M:283 W: Missing Blank Line separator, <220> field identifier  
L:94 M:283 W: Missing Blank Line separator, <400> field identifier  
L:95 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:8  
L:102 M:283 W: Missing Blank Line separator, <220> field identifier  
L:104 M:283 W: Missing Blank Line separator, <400> field identifier  
L:105 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:9  
L:112 M:283 W: Missing Blank Line separator, <220> field identifier  
L:114 M:283 W: Missing Blank Line separator, <400> field identifier  
L:115 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:10  
L:122 M:283 W: Missing Blank Line separator, <220> field identifier  
L:124 M:283 W: Missing Blank Line separator, <400> field identifier  
L:125 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:11  
L:132 M:283 W: Missing Blank Line separator, <220> field identifier  
L:134 M:283 W: Missing Blank Line separator, <400> field identifier  
L:135 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:12  
L:142 M:283 W: Missing Blank Line separator, <220> field identifier  
L:144 M:283 W: Missing Blank Line separator, <400> field identifier  
L:145 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:13  
L:152 M:283 W: Missing Blank Line separator, <220> field identifier  
L:154 M:283 W: Missing Blank Line separator, <400> field identifier  
L:155 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:14  
L:162 M:283 W: Missing Blank Line separator, <220> field identifier  
L:164 M:283 W: Missing Blank Line separator, <400> field identifier  
L:165 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:21 SEQ:15

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